

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/095,385

DATE: 06/17/98
TIME: 10:43:30

INPUT SET: S26782.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

#2

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information
4
5 (i) APPLICANT: Morrison, Sherie L.
6 Chintalacharuvu, Kote R.
7
8 (ii) TITLE OF THE INVENTION: SECRETORY IMMUNOGLOBULIN PRODUCED
9 BY SINGLE CELLS AND METHODS FOR MAKING AND USING
10 SAME
11
12 (iii) NUMBER OF SEQUENCES: 4
13
14 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
16 (B) STREET: 11150 Santa Monica Boulevard, Suite 400
17 (C) CITY: Los Angeles
18 (D) STATE: CA
19 (E) COUNTRY: USA
20 (F) ZIP: 90025
21
22 (v) COMPUTER READABLE FORM:
23 (A) MEDIUM TYPE: Diskette
24 (B) COMPUTER: IBM Compatible
25 (C) OPERATING SYSTEM: DOS
26 (D) SOFTWARE: FastSEQ for Windows Version 2.0
27
28 (vi) CURRENT APPLICATION DATA:
29 (A) APPLICATION NUMBER:
30 (B) FILING DATE: 09-JUN-1998
31 (C) CLASSIFICATION:
32
33 (vii) PRIOR APPLICATION DATA:
34 (A) APPLICATION NUMBER: 60/050,969
35 (B) FILING DATE: 19-JUN-1997
36
37
38 (viii) ATTORNEY/AGENT INFORMATION:
39 (A) NAME: Canady, Karen S
40 (B) REGISTRATION NUMBER: 39,927
41 (C) REFERENCE/DOCKET NUMBER: 30435.45USU1
42
43
44 (ix) TELECOMMUNICATION INFORMATION:
45 (A) TELEPHONE: 310 445-1140
46 (B) TELEFAX: 310 445-9031

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/095,385DATE: 06/17/98
TIME: 10:43:31

INPUT SET: S26782.raw

47 (C) TELEX:
48
49
50 (2) INFORMATION FOR SEQ ID NO:1:
51
52 (i) SEQUENCE CHARACTERISTICS:
53 (A) LENGTH: 30 base pairs
54 (B) TYPE: nucleic acid
55 (C) STRANDEDNESS: double
56 (D) TOPOLOGY: linear
57
58 (ii) MOLECULE TYPE: cDNA to mRNA
59
60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
61
62 GGGCAGAACG GTGACCATCA ACTGCCCTTT 30
63
64 (2) INFORMATION FOR SEQ ID NO:2:
65
66 (i) SEQUENCE CHARACTERISTICS:
67 (A) LENGTH: 42 base pairs
68 (B) TYPE: nucleic acid
69 (C) STRANDEDNESS: double
70 (D) TOPOLOGY: linear
71
72 (ii) MOLECULE TYPE: cDNA to mRNA
73
74 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
75
76 AAGGAATTCC TACTCTGCAA AAAGCCTGGG GTCCTGAATG GC 42
77
78 (2) INFORMATION FOR SEQ ID NO:3:
79
80 (i) SEQUENCE CHARACTERISTICS:
81 (A) LENGTH: 1839 base pairs
82 (B) TYPE: nucleic acid
83 (C) STRANDEDNESS: double
84 (D) TOPOLOGY: linear
85
86 (ii) MOLECULE TYPE: cDNA to mRNA
87
88 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
89
90 ATGCTGCTCT TCGTGCTCAC CTGCCTGCTG GCGGTCTTCC CAGCCATCTC CACGAAGAGT 60
91 CCCATATTTG GTCCCGAGGA GGTGAATAGT GTGGAAGGTA ACTCAGTGTC CATCACGTGC 120
92 TACTACCCAC CCACCTCTGT CAACCGGCAC ACCCGGAAGT ACTGGTGCCG GCAGGGAGCT 180
93 AGAGGTGGCT GCATAACCCT CATCTCCTCG GAGGGCTACG TCTCCAGCAA ATATGCAGGC 240
94 AGGGCTAACC TCACCAACTT CCCGGAGAAC GGCACATTTG TGGTGAACAT TGCCCAGCTG 300
95 AGCCAGGATG ACTCCGGGCG CTACAAGTGT GGCCTGGGCA TCAATAGCCG AGGCCTGTCC 360
96 TTTGATGTCA GCCTGGAGGT CAGCCAGGGT CCTGGGCTCC TAAATGACAC TAAAGTCTAC 420
97 ACAGTGGACC TGGGCAGAAC GGTGACCATC AACTGCCCTT TCAAGACTGA GAATGCTCAA 480
98 AAGAGGAAGT CCTTGTACAA GCAGATAGGC CTGTACCCTG TGCTGGTCAT CGACTCCAGT 540
99 GGTATGTGA ATCCCAACTA TACAGGAAGA ATACGCCTTG ATATTCAGGG TACTGGCCAG 600

RAW SEQUENCE LISTING PATENT APPLICATION US/09/095,385

DATE: 06/17/98
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100 T T A C T G T T C A G C G T T G T C A T C A A C C A A C T C A G G C T C A G C G A T G C T G G G C A G T A T C T C T G C 660
101 C A G G C T G G G G A T G A T T C C A A T A G T A A T A A G A A G A A T G C T G A C C T C C A A G T G C T A A A G C C C 720
102 G A G C C C G A G C T G G T T T A T G A A G A C C T G A G G G G C T C A G T G A C C T T C C A C T G T G C C C T G G G C 780
103 C C T G A G G T G G C A A A C G T G G C C A A A T T T C T G T G C C G A C A G A G C A G T G G G G A A A A C T G T G A C 840
104 G T G G T C G T C A A C A C C C T G G G G A A G A G G G G C C C A G C C T T T G A G G G C A G G A T C C T G C T C A A C 900
105 C C C C A G G A C A A G G A T G G C T C A T T C A G T G T G T G A T C A C A G G C C T G A G G A A G G A G G A T G C A 960
106 G G G C G C T A C C T G T G T G G A G C C A T T C G G A T G G T C A G C T G C A G G A A G G C T C G C C T A T C C A G 1020
107 G C C T G G C A A C T C T T C G T C A A T G A G G A G T C C A C G A T T C C C C G C A G C C C C A C T G T G G T G A A G 1080
108 G G G G T G G C A G G A A G C T C T G T G G C C G T G C T C T G C C C C T A C A C C G T A A G G A A A G C A A A A G C 1140
109 A T C A A G T A C T G G T G T C T C T G G A A G G G G C C C A G A A T G G C C G C T G C C C C C T G C T G G T G G A C 1200
110 A A C G A G G G G T G G G T T A A G G C C C A G T A C G A G C T C A C C A G C C G G C G C C C T G C T G G A G G A C C A G G C 1260
111 A A C G G C A C C T T C A C T G T C A T C C T C A A C C A G C T C A C C A G C C G G G A C G C C G C C T T C C C T A C T G G 1320
112 T G T C T G A C C A A C G G C G A T A C T C T C T G G A G G A C C A C C G T G G A G A T C A A G A T T A T C G A A G G A 1380
113 G A A C C A A A C C T C A A G G T A C C A G G G A A T G T C A C G G C T G T G C T G G G A G A G A C T C T C A A G G T C 1440
114 C C C T G T C A C T T T C C A T G C A A A T T C T C C T C G T A C G A G A A A T A C T G G T G C A A G T G G A A T A A C 1500
115 A C G G G C T G C C A G G C C C T G C C C A G C C A A G A C G A A G G C C C C A G C A A G G C C T T C G T G A A C T G T 1560
116 G A C G A G A A C A G C C G G C T T G T C T C C C T G A C C C T G A A C C T G G T G A C C A G G G C T G A T G A G G G C 1620
117 T G G T A C T G G T G T G G A G T G A A G C A G G G C C A C T T C T A T G G A G A G A C T G C A G C C G T C T A T G T G 1680
118 G C A G T T G A A G A G A G G A A G G C A G C G G G G T C C C G C G A T G T C A G C C T A G C G A A G G C A G A C G C T 1740
119 G C T C C T G A T G A G A A G G T G C T A G A C T C T G G T T T T C G G G A G A T T G A G A A C A A A G C C A T T C A G 1800
120 G A T C C C A G G C T T T T T G C A G A G T A G G A A T T C C T G C A G C C C 1839

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 608 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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134 Met Leu Leu Phe Val Leu Thr Cys Leu Leu Ala Val Phe Pro Ala Ile
135 1 5 10 15
136 Ser Thr Lys Ser Pro Ile Phe Gly Pro Glu Glu Val Asn Ser Val Glu
137 20 25 30
138 Gly Asn Ser Val Ser Ile Thr Cys Tyr Tyr Pro Pro Thr Ser Val Asn
139 35 40 45
140 Arg His Thr Arg Lys Tyr Trp Cys Arg Gln Gly Ala Arg Gly Gly Cys
141 50 55 60
142 Ile Thr Leu Ile Ser Ser Glu Gly Tyr Val Ser Ser Lys Tyr Ala Gly
143 65 70 75 80
144 Arg Ala Asn Leu Thr Asn Phe Pro Glu Asn Gly Thr Phe Val Val Asn
145 85 90 95
146 Ile Ala Gln Leu Ser Gln Asp Asp Ser Gly Arg Tyr Lys Cys Gly Leu
147 100 105 110
148 Gly Ile Asn Ser Arg Gly Leu Ser Phe Asp Val Ser Leu Glu Val Ser
149 115 120 125
150 Gln Gly Pro Gly Leu Leu Asn Asp Thr Lys Val Tyr Thr Val Asp Leu
151 130 135 140
152 Gly Arg Thr Val Thr Ile Asn Cys Pro Phe Lys Thr Glu Asn Ala Gln

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RAW SEQUENCE LISTING PATENT APPLICATION US/09/095,385

DATE: 06/17/98
TIME: 10:43:34

INPUT SET: S26782.raw

153	145	150	155	160
154	Lys Arg Lys Ser Leu Tyr Lys Gln Ile Gly Leu Tyr Pro Val Leu Val			
155	165	170	175	
156	Ile Asp Ser Ser Gly Tyr Val Asn Pro Asn Tyr Thr Gly Arg Ile Arg			
157	180	185	190	
158	Leu Asp Ile Gln Gly Thr Gly Gln Leu Leu Phe Ser Val Val Ile Asn			
159	195	200	205	
160	Gln Leu Arg Leu Ser Asp Ala Gly Gln Tyr Leu Cys Gln Ala Gly Asp			
161	210	215	220	
162	Asp Ser Asn Ser Asn Lys Lys Asn Ala Asp Leu Gln Val Leu Lys Pro			
163	225	230	235	240
164	Glu Pro Glu Leu Val Tyr Glu Asp Leu Arg Gly Ser Val Thr Phe His			
165	245	250	255	
166	Cys Ala Leu Gly Pro Glu Val Ala Asn Val Ala Lys Phe Leu Cys Arg			
167	260	265	270	
168	Gln Ser Ser Gly Glu Asn Cys Asp Val Val Val Asn Thr Leu Gly Lys			
169	275	280	285	
170	Arg Ala Pro Ala Phe Glu Gly Arg Ile Leu Leu Asn Pro Gln Asp Lys			
171	290	295	300	
172	Asp Gly Ser Phe Ser Val Ile Thr Gly Leu Arg Lys Glu Asp Ala			
173	305	310	315	320
174	Gly Arg Tyr Leu Cys Gly Ala His Ser Asp Gly Gln Leu Gln Glu Gly			
175	325	330	335	
176	Ser Pro Ile Gln Ala Trp Gln Leu Phe Val Asn Glu Glu Ser Thr Ile			
177	340	345	350	
178	Pro Arg Ser Pro Thr Val Val Lys Gly Val Ala Gly Ser Ser Val Ala			
179	355	360	365	
180	Val Leu Cys Pro Tyr Asn Arg Lys Glu Ser Lys Ser Ile Lys Tyr Trp			
181	370	375	380	
182	Cys Leu Trp Glu Gly Ala Gln Asn Gly Arg Cys Pro Leu Leu Val Asp			
183	385	390	395	400
184	Ser Glu Gly Trp Val Lys Ala Gln Tyr Glu Gly Arg Leu Ser Leu Leu			
185	405	410	415	
186	Glu Glu Pro Gly Asn Gly Thr Phe Thr Val Ile Leu Asn Gln Leu Thr			
187	420	425	430	
188	Ser Arg Asp Ala Gly Phe Tyr Trp Cys Leu Thr Asn Gly Asp Thr Leu			
189	435	440	445	
190	Trp Arg Thr Thr Val Glu Ile Lys Ile Ile Glu Gly Glu Pro Asn Leu			
191	450	455	460	
192	Lys Val Pro Gly Asn Val Thr Ala Val Leu Gly Glu Thr Leu Lys Val			
193	465	470	475	480
194	Pro Cys His Phe Pro Cys Lys Phe Ser Ser Tyr Glu Lys Tyr Trp Cys			
195	485	490	495	
196	Lys Trp Asn Asn Thr Gly Cys Gln Ala Leu Pro Ser Gln Asp Glu Gly			
197	500	505	510	
198	Pro Ser Lys Ala Phe Val Asn Cys Asp Glu Asn Ser Arg Leu Val Ser			
199	515	520	525	
200	Leu Thr Leu Asn Leu Val Thr Arg Ala Asp Glu Gly Trp Tyr Trp Cys			
201	530	535	540	
202	Gly Val Lys Gln Gly His Phe Tyr Gly Glu Thr Ala Ala Val Tyr Val			
203	545	550	555	560
204	Ala Val Glu Glu Arg Lys Ala Ala Gly Ser Arg Asp Val Ser Leu Ala			
205	565	570	575	

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PATENT APPLICATION US/09/095,385DATE: 06/17/98
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INPUT SET: S26782.raw

206	Lys	Ala	Asp	Ala	Ala	Pro	Asp	Glu	Lys	Val	Leu	Asp	Ser	Gly	Phe	Arg
207				580					585					590		
208	Glu	Ile	Glu	Asn	Lys	Ala	Ile	Gln	Asp	Pro	Arg	Leu	Phe	Ala	Glu	Glx
209			595					600					605			

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/095,385

DATE: 06/17/98
TIME: 10:43:35

INPUT SET: S26782.raw

Line

Error

Original Text